



1600

RAW SEQUENCE LISTING

DATE: 11/07/2003

PATENT APPLICATION: US/09/826,115A

TIME: 14:27:33

Input Set : A:\64908 seq.txt

Output Set: N:\CRF4\11062003\I826115A.raw

3 <110> APPLICANT: The Government of the United States of America, as
 4 represented by the Secretary, Department of Health and Human
 5 Services, c/o Centers for Disease Control and Prevention
 6 Chang, Gwong-Jen J.
 8 <120> TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
 10 <130> FILE REFERENCE: 6395-64908
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/826,115A
 C--> 12 <141> CURRENT FILING DATE: 2001-04-04
 12 <150> PRIOR APPLICATION NUMBER: PCT/US02/10764
 13 <151> PRIOR FILING DATE: 2002-04-04
 15 <150> PRIOR APPLICATION NUMBER: 09/826,115
 16 <151> PRIOR FILING DATE: 2001-04-04
 18 <150> PRIOR APPLICATION NUMBER: 09/701,536
 19 <151> PRIOR FILING DATE: 2000-11-29
 21 <150> PRIOR APPLICATION NUMBER: PCT/US99/12298
 22 <151> PRIOR FILING DATE: 1999-06-03
 24 <150> PRIOR APPLICATION NUMBER: 60/087,908
 25 <151> PRIOR FILING DATE: 1998-06-04
 27 <160> NUMBER OF SEQ ID NOS: 61
 29 <170> SOFTWARE: PatentIn version 3.2
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 48
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Artificial Sequence
 36 <220> FEATURE:
 37 <223> OTHER INFORMATION: Description of artificial sequence; note = synthetic
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 40 <220> FEATURE:
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 42 <222> LOCATION: (1)..(48)
 43 <223> OTHER INFORMATION: Amplimer 14DV389
 45 <220> FEATURE:
 46 <221> NAME/KEY: CDS
 47 <222> LOCATION: (25)..(48)
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 51 Met Gly Arg Lys Gln Asn Lys Arg
 52 1 5
 55 <210> SEQ ID NO: 2
 56 <211> LENGTH: 8
 57 <212> TYPE: PRT
 58 <213> ORGANISM: Artificial Sequence
 60 <220> FEATURE:
 61 <223> OTHER INFORMATION: Description of artificial sequence; note = synthetic

ENTERED

construct

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66 1 5
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80 <222> LOCATION: (1)..(50)
81 <223> OTHER INFORMATION: Amplimer c14DV2453
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98 <222> LOCATION: (1)..(48)
99 <223> OTHER INFORMATION: Amplimer YFDV389
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136 <222> LOCATION: (1)..(41)
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155 <223> OTHER INFORMATION: Amplimer SLEDV410
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159 <222> LOCATION: (25)..(51)
161 <400> SEQUENCE: 7
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164 1 5
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168 <211> LENGTH: 9
169 <212> TYPE: PRT
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193 <223> OTHER INFORMATION: Amplimer cSLEDV2449
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205 <223> OTHER INFORMATION: Description of artificial sequence; note = synthetic
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211 <223> OTHER INFORMATION: pCDJE 2-7
213 <220> FEATURE:
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215 <222> LOCATION: (916)..(3009)
217 <400> SEQUENCE: 10
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220 ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg      120
222 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
224 ttaggggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
226 gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata      300
228 tggagttccg cgttacataa cttacggtaa atggcccggc tggctgaccg cccaacgacc      360
230 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgcccaata gggactttcc      420
232 attgacgtca atgggtggac tatttacggg aaactgccc cttggcagta catcaagtgt      480
234 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
236 atgccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca      600
238 tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660
240 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc      720
242 aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg      780
244 gtaggcgtgt acgggtgggag gtctatataa gcagagctct ctggctaact agagaaccca      840
246 ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttgggtacc      900
248 gagctcgccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa      951
249           Met Gly Arg Lys  Gln Asn Lys Arg Gly Gly Asn Glu
250           1           5           10
252 ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg      999
253 Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
254           15           20           25
256 gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc      1047
257 Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
258           30           35           40
260 aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga      1095
261 Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
262 45           50           55           60
264 gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag      1143
265 Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
266           65           70           75
268 gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca      1191
269 Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
270           80           85           90
272 gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat      1239
273 Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr
274           95           100           105
276 gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg      1287
277 Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val
278           110           115           120
280 tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct      1335
281 Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala
282 125           130           135           140

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284 tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac      1383
285 Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn
286          145          150          155
288 tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc      1431
289 Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly
290          160          165          170
292 tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc      1479
293 Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu
294          175          180          185
296 ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc      1527
297 Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly
298          190          195          200
300 aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg      1575
301 Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu
302 205          210          215          220
304 gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca      1623
305 Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro
306          225          230          235
308 aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag      1671
309 Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu
310          240          245          250
312 gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg      1719
313 Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val
314          255          260          265
316 gct cgg tgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat      1767
317 Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp
318          270          275          280
320 agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac      1815
321 Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn
322 285          290          295          300
324 gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc      1863
325 Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe
326          305          310          315
328 tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc      1911
329 Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile
330          320          325          330
332 aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac      1959
333 Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn
334          335          340          345
336 cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt      2007
337 His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe
338          350          355          360
340 aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac      2055
341 Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr
342 365          370          375          380
344 gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa      2103
345 Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu
346          385          390          395
348 gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg      2151

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date